

10/566851

SEQUENCE LISTING

JAP20 Rec'd PCT/PTO 01 FEB 2006

<110> Jacquemin, Marc
Saint-Remy, Jean-Marie

<120> Variable antibodies

<130> 50304/112001

<150> GB 0319118.6
<151> 2003-08-14

<150> GB 0319345.5
<151> 2003-08-18

<160> 32

<170> PatentIn version 3.3

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Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

48

gcc cac tcc cag gtg caa ctg gtg caa tct ggg gct gag gtg aag aag
Ala His Ser Gln Val Gln Ser Gly Ala Glu Val Lys Lys

96

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cct ggg gcc tca gtg aag gtc tcc tgc aag acc tct gga tac aac ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe			144
35	40	45	
acc ggc tac tct gct tct gga cat atc ttc acc gcc tac tct gtg cac Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His			192
50	55	60	
tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga agg atc Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile			240
65	70	75	80
aac cct aac agt ggt gcc aca gac tat gca cat aaa ttt cag ggc agg Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg			288
85	90	95	
gtc acc atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu			336
100	105	110	
agc agg ctg aca tct gac gac acg gcc atg tat tac tgt gcg aga gcc Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala			384
115	120	125	
gac aac tat ttc gat att gtg act ggc tat act tct cat tac ttt gac Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp			432
130	135	140	
tac tgg ggc cgg gga acc ctg gtc acc gtc tcc tca gcc tcc acc aag Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys			480
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ggc cca tcg gtc ttc c Gly Pro Ser Val Phe			496
165			

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Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe
35 40 45

Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His
50 55 60

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile
65 70 75 80

Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg
85 90 95

Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu
100 105 110

Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala
115 120 125

Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp
130 135 140

Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
145 150 155 160

Gly Pro Ser Val Phe
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1 5 10 15

gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct 96
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
20 25 30

ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa cct ggc cag gct 192
Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca 240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
65 70 75 80

cac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc 288
His Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

agc aga ctg gag cct gaa gat ttt gca gtg tac tac tgt cag caa tat 336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

ggt acc tca gcc tta ctc act ttc ggc gga ggg acc aag gtg gag atc 384
Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Thr Lys Val Glu Ile
115 120 125

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<213> Homo sapiens

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25

30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
65 70 75 80

His Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Thr Lys Val Glu Ile
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
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<223> Krix-1 heavy chain forward primer

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<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Krix-1 heavy chain reverse primer

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<210> 8
<211> 36
<212> DNA
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<220>
<223> Krix-1 light chain reverse primer

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<210> 10
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<210> 11
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<223> Krix-1 reverse mutagenic primer Asn47Asp

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<210> 24
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gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser	20	25	30		96
ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser	35	40	45		144
gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa cct ggc cag gct Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala	50	55	60		192
ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro	65	70	75	80	240
cac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc His Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile	85	90	95		288
agc aga ctg gag cct gaa gat ttt gca gtg tac tac tgt cag caa tat Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr	100	105	110		336
ggt acc tca gcc tta ctc act ttc ggc gga ggg acc aag gtg gag atc Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Thr Lys Val Glu Ile	115	120	125		384
aaa cga ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga Lys Arg Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly	130	135	140		432
tcg cag gta cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly	145	150	155	160	480
gcc tca gtg aag gtc tcc tgc aag acc tct gga tac caa ttc acc ggc Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Gln Phe Thr Gly	165	170	175		528
tac tct gct tct gga cat atc ttc acc gcc tac tct gtg cac tgg gtg Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His Trp Val	180	185	190		576
cga cag gcc cct gga caa ggg ctt gag tgg atg gga agg atc aac cct Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro	195	200	205		624
aac agt ggt gcc aca gac tat gca cat aaa ttt cag ggc agg gtc acc Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg Val Thr	210	215	220		672
atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg agc agg					720

Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg			
225	230	235	240
ctg aca tct gac gac aca gcc atg tat tac tgt gcg aga gcc gac aac			768
Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala Asp Asn			
245	250	255	
tat ttc gat att gtg act ggc tat act tct cat tac ttt gac tac tgg			816
Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp Tyr Trp			
260	265	270	
ggc cgg gga acc ctg gtc acc gtc tcc tca cat cat cat cat cat cat			864
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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser			
35	40	45	

Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala			
50	55	60	

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro			
65	70	75	80

His Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile			
85	90	95	

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr			
100	105	110	

Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Thr Lys Val Glu Ile

115

120

125

Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
145 150 155 160

Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Gln Phe Thr Gly
165 170 175

Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His Trp Val
180 185 190

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro
195 200 205

Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg Val Thr
210 215 220

Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg
225 230 235 240

Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala Asp Asn
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Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp Tyr Trp
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Gly Arg Gly Thr Leu Val Thr Val Ser Ser His His His His His His
275 280 285

<210> 27

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<212> DNA

<213> Artificial Sequence

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<210> 28

<211> 54

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gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag      96
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20          25          30

ccc ggg tcg tcg gtg atg gtc tcc tgc aag gct tct gga ggc acc ttc      144
Pro Gly Ser Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
35          40          45

agc agc ttt ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt      192
Ser Ser Phe Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50          55          60

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65 70 75 80	
cgg aac ttc cag aat aga gtc acc att acc gcg gac gaa ttc acg agc	288
Arg Asn Phe Gln Asn Arg Val Thr Ile Thr Ala Asp Glu Phe Thr Ser	
85 90 95	
aca gcc tac ata cga ctg agg agc ctg aga tct gaa gat acg gcc gtg	336
Thr Ala Tyr Ile Arg Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gtc ggc ggt cga gat gcc tac agc ttt gat ggt ttt gat	384
Tyr Tyr Cys Val Gly Gly Arg Asp Ala Tyr Ser Phe Asp Gly Phe Asp	
115 120 125	
gtc tgg ggc caa ggg aca atg gtc acc gtc tct tca gcc tcc acc aag	432
Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys	
130 135 140	
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Gly Pro Ser Val Phe Pro	
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Pro Gly Ser Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe	
35 40 45	
Ser Ser Phe Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
50 55 60	
Glu Trp Val Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Thr Ala	
65 70 75 80	
Arg Asn Phe Gln Asn Arg Val Thr Ile Thr Ala Asp Glu Phe Thr Ser	
85 90 95	

Thr Ala Tyr Ile Arg Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Val Gly Gly Arg Asp Ala Tyr Ser Phe Asp Gly Phe Asp
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Ser Val Ala Ser Ser Gly Leu Thr Gln Pro His Ser Val Ser Val Ser
20 25 30

cca gga cag aca gcc aac atc acc tgc tct aga gat aag ttg ggt cat 144

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aaa ttt gct tcc tgg tat caa cag aag cca ggc cag tcc cct gct ctt															192	
Lys	Phe	Ala	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Ala	Leu	
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ctc atc tat caa gac agc aag cgg ccc tca ggg atc cct gag cga ttc															240	
Leu	Ile	Tyr	Gln	Asp	Ser	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	
65																80
tct ggc tcc aac tct ggg aac aca gcc act ctg acc atc agc ggg acc															288	
Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Thr	
85																95
cag gct atg gat gag gct gac tat tac tgt cag gcg tgg gac aac acc															336	
Gln	Ala	Met	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ala	Trp	Asp	Asn	Thr	
100																110
act gcc gta ttc ggc gga ggg acc aag ttg aca gtc cta agt cag ccc															384	
Thr	Ala	Val	Phe	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Gln	Pro		
115																125
aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc															420	
Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser					
130																140
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Ser Val Ala Ser Ser Gly Leu Thr Gln Pro His Ser Val Ser Val Ser																
20																30
Pro Gly Gln Thr Ala Asn Ile Thr Cys Ser Arg Asp Lys Leu Gly His																
35																45
Lys Phe Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Ala Leu																
50																60
Leu Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe																
65																80
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr																
85																95

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Asn Thr
100 105 110

Thr Ala Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
115 120 125

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
130 135 140